



IFW16

RAW SEQUENCE LISTING

DATE: 08/16/2004

PATENT APPLICATION: US/10/026,331B

TIME: 09:38:59

Input Set : A:\-13-1.app

Output Set: N:\CRF4\08162004\J026331B.raw

3 <110> APPLICANT: Hitoshi, Yasumichi
 4 Demo, Susan
 5 Jenkins, Yonchu
 6 Rigel Pharmaceuticals, Inc.
 8 <120> TITLE OF INVENTION: MRE11: Modulation of Cellular Proliferation
 10 <130> FILE REFERENCE: 021044-001310US
 12 <140> CURRENT APPLICATION NUMBER: US 10/026,331B
 13 <141> CURRENT FILING DATE: 2001-12-21
 15 <150> PRIOR APPLICATION NUMBER: US 60/309,737
 16 <151> PRIOR FILING DATE: 2001-08-01
 18 <160> NUMBER OF SEQ ID NOS: 21
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2537
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
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 28 <223> OTHER INFORMATION: human MRE11 meiotic recombination 11 homolog A
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (171)..(2297)
 33 <223> OTHER INFORMATION: MRE11
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 38 gggttcttg agaagaacct ggtcccagag gagcttgact gaccataaaa atgagtactg 180
 39 cagatgcact tgatgatgaa aacacattta aaatattagt tgcaacagat attcatcttg 240
 40 gatttatgga gaaagatgca gtcagaggaa atgatacggt tgtaacactc gatgaaattt 300
 41 taagacttgc ccaggaaaat gaagtggatt ttattttggt aggtgggtgat ctttttcatg 360
 42 aaaataagcc ctcaaggaaa acattacata cctgcctcga gttattaaga aaatattgta 420
 43 tgggtgatcg gcctgtccag tttgaaattc tcagtgatca gtcagtcaac tttggtttta 480
 44 gtaagtttcc atgggtgaac tatcaagatg gcaacctcaa catttcaatt ccagtgttta 540
 45 gtattcatgg caatcatgac gatcccacag gggcagatgc actttgtgcc ttggacattt 600
 46 taagttgtgc tggatttgta aatcactttg gacgttcaat gtctgtggag aagatagaca 660
 47 ttagtccggt tttgcttcaa aaaggaagca caaagattgc gctatatggt ttaggatcca 720
 48 ttccagatga aaggctctat cgaatgtttg tcaataaaaa agtaacaatg ttgagaccaa 780
 49 aggaagatga gaactcttgg tttaacttat ttgtgattca tcagaacagg agtaaacatg 840
 50 gaagtactaa cttcattcca gaacaatttt tggatgactt cattgatctt gttatctggg 900
 51 gccatgaaca tgagtgtaaa atagctccaa ccaaaaatga acaacagctg ttttatatct 960
 52 cacaacctgg aagctcagtg gttacttctc tttcccagg agaagctgta aagaaacatg 1020
 53 ttggtttgct gcgtattaaa gggaggaaga tgaatatgca taaaattcct cttcacacag 1080
 54 tgcggcagtt tttcatggag gatattgttc tagctaata tccagacatt ttaaccag 1140
 55 ataactctaa agtaacccaa gccatacaaa gcttctgttt ggagaagatt gaagaaatgc 1200



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56 ttgaaaatgc tgaacgggaa cgtctgggta attctcacca gccagagaag cctcttgtag 1260
57 gactgcgagt ggactatagt ggaggttttg aacctttcag tgttcttcgc tttagccaga 1320
58 aatttggtga tcgggtagct aatccaaaag acattatcca ttttttcagg catagagaac 1380
59 aaaaggaaaa aacaggagaa gagatcaact ttgggaaact tatcacaag ccttcagaag 1440
60 gaacaacttt aagggtagaa gatcttgtaa aacagtactt tcaaaccgca gagaagaatg 1500
61 tgcagctctc actgctaaca gaaagaggga tgggtgaagc agtacaagaa tttgtggaca 1560
62 aggaggagaa agatgccatt gaggaattag tgaaatacca gttggaaaaa acacagcgat 1620
63 ttcttaaaga acgtcatatt gatgccctcg aagacaaaat cgatgaggag gtacgtcggt 1680
64 tcagagaaac cagacaaaaa aatactaatt agaagatga tgaagtccgt gaggctatga 1740
65 ccaggggccag agcactcaga tctcagtcag aggagtctgc ttctgccttt agtgctgatg 1800
66 accttatgag tatagattta gcagaacaga tggctaata ga ctctgatgat agcatctcag 1860
67 cagcaaccaa caaaggaaga ggccgaggaa gaggtcgaag aggtggaaga gggcagaatt 1920
68 cagcatcgag aggagggtct caaagaggaa gagcagacac tgggtctggag acttctaccc 1980
69 gtagcaggaa ctcaaagact gctgtgtcag catctagaaa tatgtctatt atagatgcct 2040
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71 ttgaggtaga tgaatcagat gtggaagaag acatttttcc taccacttca aagacagatc 2160
72 aaaggtggtc cagcacatca tccagcaaaa tcatgtccca gagtcaagta tcgaaagggg 2220
73 ttgattttga atcaagtga gatgatgat atgatccttt tatgaacact agttctttta 2280
74 gaagaaatag aagataatat atttaatggc actgagaaac atgcaagata caggaaaaat 2340
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76 actccataag taagaaatct ctagtccaca gacatacaat agcattgatt caccttggtt 2460
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81 <210> SEQ ID NO: 2

82 <211> LENGTH: 708

83 <212> TYPE: PRT

84 <213> ORGANISM: Homo sapiens

86 <220> FEATURE:

87 <223> OTHER INFORMATION: human MRE11 meiotic recombination 11 homolog A

89 <400> SEQUENCE: 2

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92 Val Ala Thr Asp Ile His Leu Gly Phe Met Glu Lys Asp Ala Val Arg
93             20             25             30
94 Gly Asn Asp Thr Phe Val Thr Leu Asp Glu Ile Leu Arg Leu Ala Gln
95             35             40             45
96 Glu Asn Asp Glu Val Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu
97             50             55             60
98 Asn Lys Pro Ser Arg Lys Thr Leu His Thr Cys Leu Glu Leu Leu Arg
99   65             70             75             80
100 Lys Tyr Cys Met Gly Asp Arg Pro Val Gln Phe Glu Ile Leu Ser Asp
101             85             90             95
102 Gln Ser Val Asn Phe Gly Phe Ser Lys Phe Pro Trp Val Asn Tyr Gln
103             100            105            110
104 Asp Gly Asn Leu Asn Ile Ser Ile Pro Val Phe Ser Ile His Gly Asn
105             115            120            125
106 His Asp Asp Pro Thr Gly Ala Asp Ala Leu Cys Ala Leu Asp Ile Leu
107             130            135            140
108 Ser Cys Ala Gly Phe Val Asn His Phe Gly Arg Ser Met Ser Val Glu

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109 145          150          155          160
110 Lys Ile Asp Ile Ser Pro Val Leu Leu Gln Lys Gly Ser Thr Lys Ile
111          165          170          175
112 Ala Leu Tyr Gly Leu Gly Ser Ile Pro Asp Glu Arg Leu Tyr Arg Met
113          180          185          190
114 Phe Val Asn Lys Lys Val Thr Met Leu Arg Pro Lys Glu Asp Glu Asn
115          195          200          205
116 Ser Trp Phe Asn Leu Phe Val Ile His Gln Asn Arg Ser Lys His Gly
117          210          215          220
118 Ser Thr Asn Phe Ile Pro Glu Gln Phe Leu Asp Asp Phe Ile Asp Leu
119 225          230          235          240
120 Val Ile Trp Gly His Glu His Glu Cys Lys Ile Ala Pro Thr Lys Asn
121          245          250          255
122 Glu Gln Gln Leu Phe Tyr Ile Ser Gln Pro Gly Ser Ser Val Val Thr
123          260          265          270
124 Ser Leu Ser Pro Gly Glu Ala Val Lys Lys His Val Gly Leu Leu Arg
125          275          280          285
126 Ile Lys Gly Arg Lys Met Asn Met His Lys Ile Pro Leu His Thr Val
127          290          295          300
128 Arg Gln Phe Phe Met Glu Asp Ile Val Leu Ala Asn His Pro Asp Ile
129 305          310          315          320
130 Phe Asn Pro Asp Asn Pro Lys Val Thr Gln Ala Ile Gln Ser Phe Cys
131          325          330          335
132 Leu Glu Lys Ile Glu Glu Met Leu Glu Asn Ala Glu Arg Glu Arg Leu
133          340          345          350
134 Gly Asn Ser His Gln Pro Glu Lys Pro Leu Val Arg Leu Arg Val Asp
135          355          360          365
136 Tyr Ser Gly Gly Phe Glu Pro Phe Ser Val Leu Arg Phe Ser Gln Lys
137          370          375          380
138 Phe Val Asp Arg Val Ala Asn Pro Lys Asp Ile Ile His Phe Phe Arg
139 385          390          395          400
140 His Arg Glu Gln Lys Glu Lys Thr Gly Glu Glu Ile Asn Phe Gly Lys
141          405          410          415
142 Leu Ile Thr Lys Pro Ser Glu Gly Thr Thr Leu Arg Val Glu Asp Leu
143          420          425          430
144 Val Lys Gln Tyr Phe Gln Thr Ala Glu Lys Asn Val Gln Leu Ser Leu
145          435          440          445
146 Leu Thr Glu Arg Gly Met Gly Glu Ala Val Gln Glu Phe Val Asp Lys
147          450          455          460
148 Glu Glu Lys Asp Ala Ile Glu Glu Leu Val Lys Tyr Gln Leu Glu Lys
149 465          470          475          480
150 Thr Gln Arg Phe Leu Lys Glu Arg His Ile Asp Ala Leu Glu Asp Lys
151          485          490          495
152 Ile Asp Glu Glu Val Arg Arg Phe Arg Glu Thr Arg Gln Lys Asn Thr
153          500          505          510
154 Asn Glu Glu Asp Asp Glu Val Arg Glu Ala Met Thr Arg Ala Arg Ala
155          515          520          525
156 Leu Arg Ser Gln Ser Glu Glu Ser Ala Ser Ala Phe Ser Ala Asp Asp
157          530          535          540

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158 Leu Met Ser Ile Asp Leu Ala Glu Gln Met Ala Asn Asp Ser Asp Asp
159 545          550          555          560
160 Ser Ile Ser Ala Ala Thr Asn Lys Gly Arg Gly Arg Gly Arg Gly Arg
161          565          570          575
162 Arg Gly Gly Arg Gly Gln Asn Ser Ala Ser Arg Gly Gly Ser Gln Arg
163          580          585          590
164 Gly Arg Ala Asp Thr Gly Leu Glu Thr Ser Thr Arg Ser Arg Asn Ser
165          595          600          605
166 Lys Thr Ala Val Ser Ala Ser Arg Asn Met Ser Ile Ile Asp Ala Phe
167          610          615          620
168 Lys Ser Thr Arg Gln Gln Pro Ser Arg Asn Val Thr Thr Lys Asn Tyr
169 625          630          635          640
170 Ser Glu Val Ile Glu Val Asp Glu Ser Asp Val Glu Glu Asp Ile Phe
171          645          650          655
172 Pro Thr Thr Ser Lys Thr Asp Gln Arg Trp Ser Ser Thr Ser Ser Ser
173          660          665          670
174 Lys Ile Met Ser Gln Ser Gln Val Ser Lys Gly Val Asp Phe Glu Ser
175          675          680          685
176 Ser Glu Asp Asp Asp Asp Asp Pro Phe Met Asn Thr Ser Ser Leu Arg
177          690          695          700
178 Arg Asn Arg Arg
179 705
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 299
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
187 <220> FEATURE:
188 <223> OTHER INFORMATION: human MRE11 amino acids 9-307
190 <400> SEQUENCE: 3
191 Asp Glu Asn Thr Phe Lys Ile Leu Val Ala Thr Asp Ile His Leu Gly
192 1          5          10          15
193 Phe Met Glu Lys Asp Ala Ala Arg Gly Asn Asp Thr Phe Val Thr Leu
194          20          25          30
195 Asp Glu Ile Leu Arg Leu Ala Gln Glu Asn Glu Val Asp Phe Ile Leu
196          35          40          45
197 Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro Ser Arg Lys Thr Leu
198          50          55          60
199 His Thr Cys Leu Glu Leu Arg Lys Tyr Cys Met Gly Asp Arg Pro
200 65          70          75          80
201 Val Gln Phe Glu Ile Leu Ser Asp Gln Ser Val Asn Phe Gly Phe Ser
202          85          90          95
203 Lys Phe Pro Trp Val Asn Tyr Gln Asp Gly Asn Leu Asn Ile Ser Ile
204          100          105          110
205 Pro Val Phe Ser Ile His Gly Asn His Asp Asp Pro Thr Gly Ala Asp
206          115          120          125
207 Ala Leu Cys Ala Leu Asp Ile Leu Ser Cys Ala Gly Phe Val Asn His
208          130          135          140
209 Phe Gly Arg Ser Met Ser Val Glu Lys Ile Asp Ile Ser Pro Val Leu
210 145          150          155          160

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211 Leu Gln Lys Gly Ser Thr Lys Ile Ala Leu Tyr Gly Leu Gly Ser Ile
212          165          170          175
213 Pro Asp Glu Arg Leu Tyr Arg Met Phe Val Asn Lys Lys Val Thr Met
214          180          185          190
215 Leu Arg Pro Lys Glu Asp Glu Asn Ser Trp Phe Asn Leu Phe Val Ile
216          195          200          205
217 His Gln Asn Arg Ser Lys His Gly Ser Thr Asn Phe Ile Pro Glu Gln
218          210          215          220
219 Phe Leu Asp Asp Phe Ile Asp Leu Val Ile Trp Gly His Glu His Glu
220 225          230          235          240
221 Cys Lys Ile Ala Pro Thr Lys Asn Glu Gln Gln Leu Phe Tyr Ile Ser
222          245          250          255
223 Gln Pro Gly Ser Ser Val Val Thr Ser Leu Ser Pro Gly Glu Ala Val
224          260          265          270
225 Lys Lys His Val Gly Leu Leu Arg Ile Lys Gly Arg Lys Met Asn Met
226          275          280          285
227 His Lys Ile Pro Leu His Thr Val Arg Gln Phe
228          290          295
231 <210> SEQ ID NO: 4
232 <211> LENGTH: 300
233 <212> TYPE: PRT
234 <213> ORGANISM: Saccharomyces cerevisiae
236 <220> FEATURE:
237 <223> OTHER INFORMATION: yeast MRE11 amino acids 5-304
239 <400> SEQUENCE: 4
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242 Tyr Asn Glu Asn Asp Pro Ile Thr Gly Asp Asp Ser Trp Lys Thr Phe
243          20          25          30
244 His Glu Val Met Met Leu Ala Lys Asn Asn Asn Val Asp Met Val Val
245          35          40          45
246 Gln Ser Gly Asp Leu Phe His Val Asn Lys Pro Ser Lys Lys Ser Leu
247          50          55          60
248 Tyr Gln Val Leu Lys Thr Leu Arg Leu Cys Cys Met Gly Asp Lys Pro
249 65          70          75          80
250 Cys Glu Leu Glu Leu Leu Ser Asp Pro Ser Gln Val Phe His Tyr Asp
251          85          90          95
252 Glu Phe Thr Asn Val Asn Tyr Glu Asp Pro Asn Phe Asn Ile Ser Ile
253          100          105          110
254 Pro Val Phe Gly Ile Ser Gly Asn His Asp Asp Ala Ser Gly Asp Ser
255          115          120          125
256 Leu Leu Cys Pro Met Asp Ile Leu His Ala Thr Gly Leu Ile Asn His
257          130          135          140
258 Phe Gly Lys Val Ile Glu Ser Asp Lys Ile Lys Val Val Pro Leu Leu
259 145          150          155          160
260 Phe Gln Lys Gly Ser Thr Lys Leu Ala Leu Tyr Gly Leu Ala Ala Val
261          165          170          175
262 Arg Asp Glu Arg Leu Phe Arg Thr Phe Lys Asp Gly Gly Val Thr Phe
263          180          185          190

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/026,331B

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Input Set : A:\-13-1.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 5,7,9
Seq#:7; Xaa Pos. 5
Seq#:8; Xaa Pos. 2
Seq#:12; Xaa Pos. 1,6
Seq#:13; Xaa Pos. 7
Seq#:14; Xaa Pos. 5
Seq#:16; Xaa Pos. 2
Seq#:17; Xaa Pos. 3,5
Seq#:19; N Pos. 1,27,40

VERIFICATION SUMMARY

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Input Set : A:\-13-1.app

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L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0